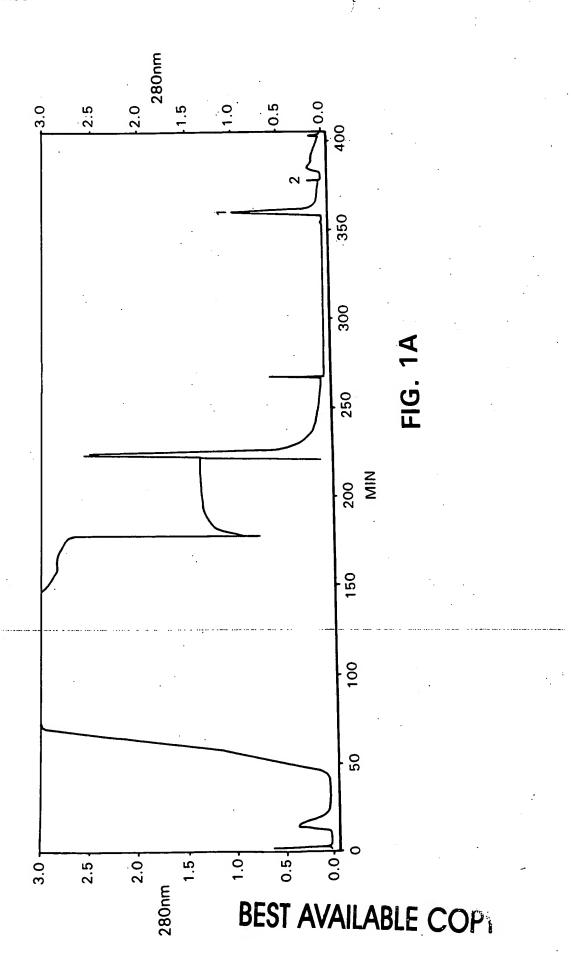
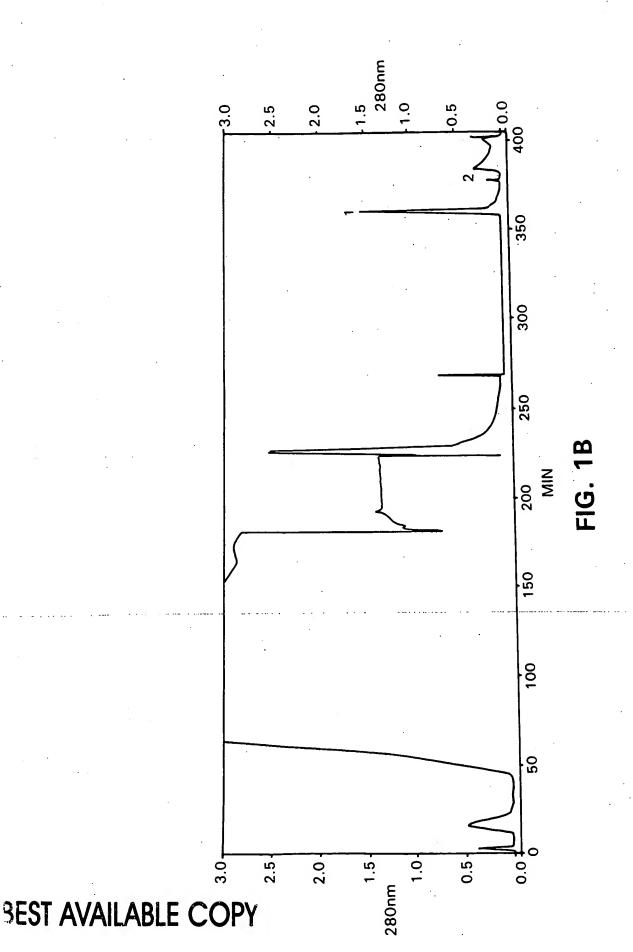
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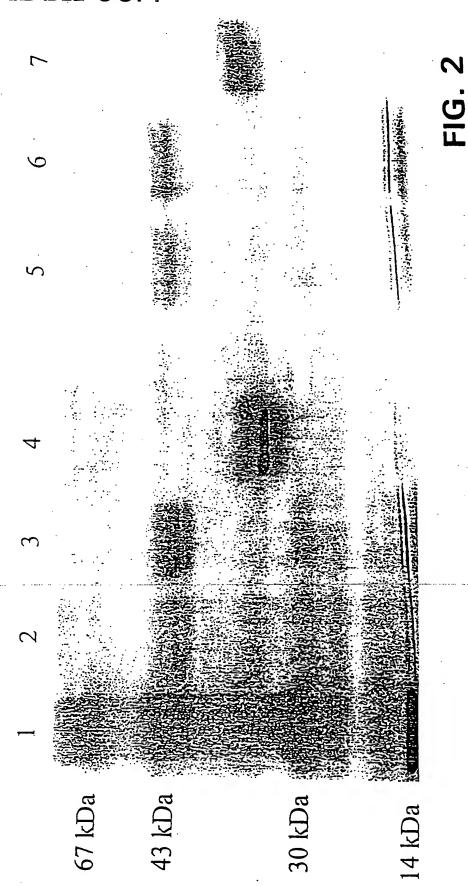
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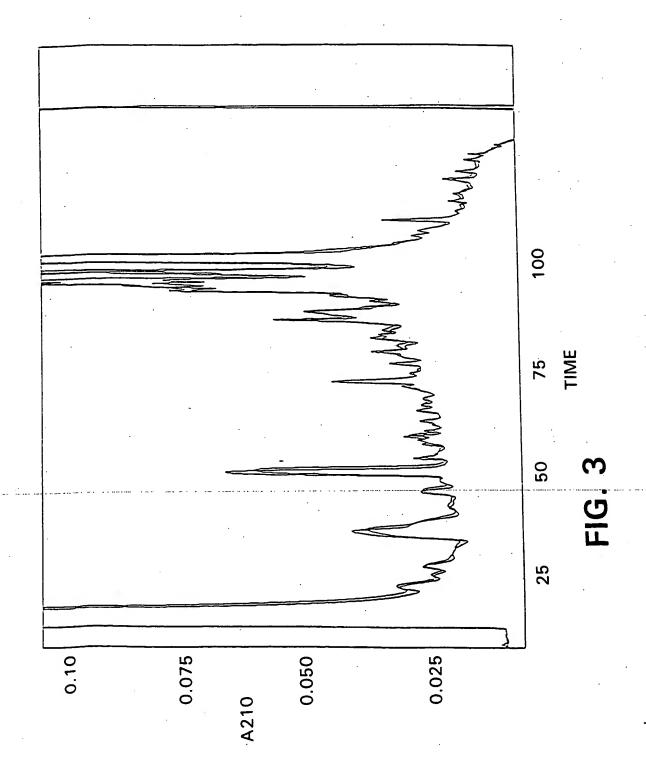
Matter No.: 08191-008004 Page 2 of 10 Applicant(s): Roman M. Chicz et al.

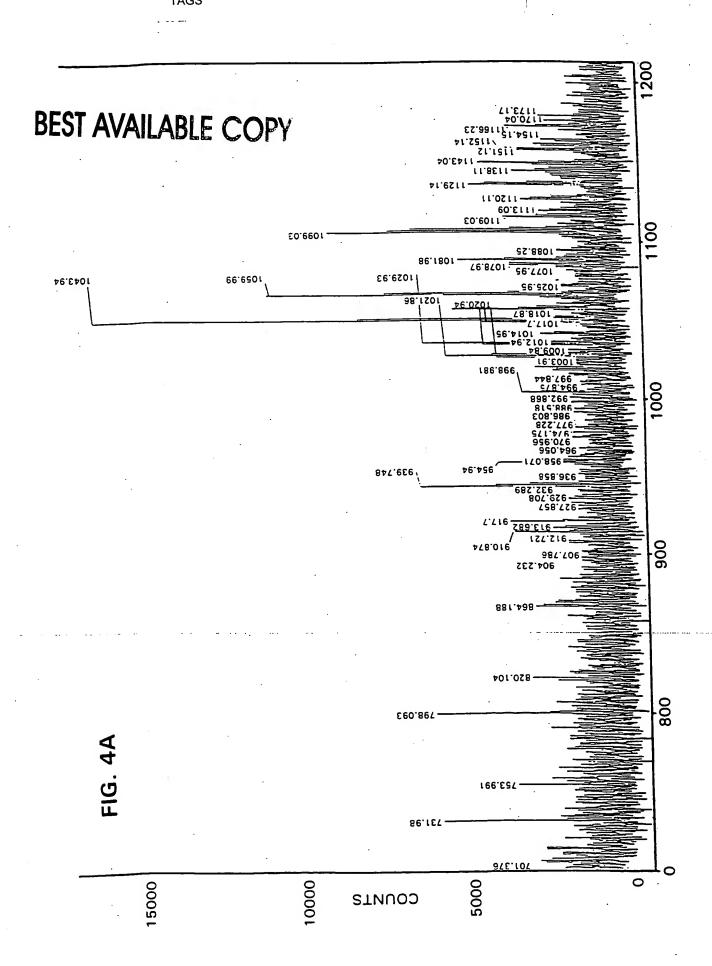
Applicant(s): Roman M. Chicz et al.
PROFILING AND CATALOGING EXPRESSED PROTEIN
TAGS



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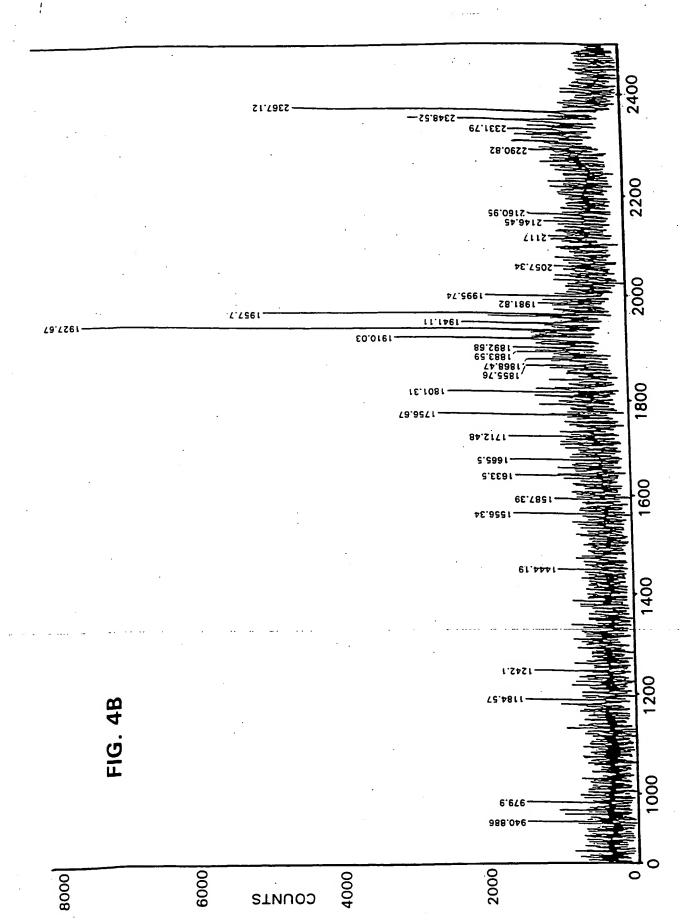
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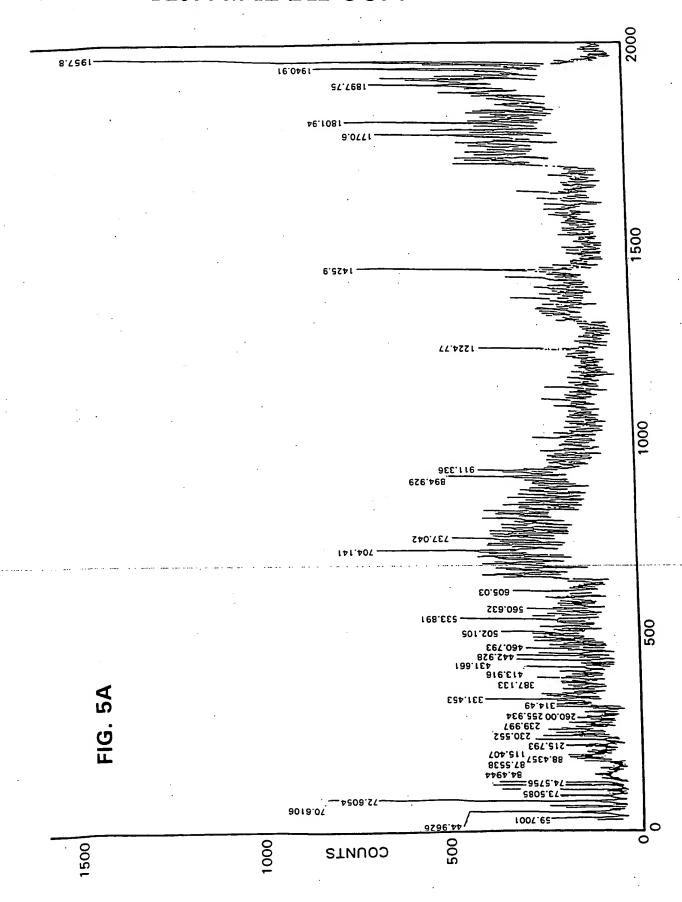
Matter No.: 08191-008004

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**TAGS** 



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**TAGS** 

Sample ID (comment): R4A3F37m1957
Database searched: NCBInr.7.5.97
Molecular weight search (1000-100000 Da) selects 269572 entries.
Species search (HOMO SAPIENS) selects 22771 entries.
Combined molecular weight and species searches select 20933 entries.
Number of sequences passing through parent mass filter: 84015

search selects 257 entries

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		Protein Name	(D82930) HI.A-A26-varient	(U25971) MHC class 1 antigen HLA-A2407	(X82161) HLA-A alphal and alpha2 domains	(D32129) HLA-A26	(297370) human feukocyte antigen	(U18930)MHC class 1 antigen HLA-A2	(M160010) HLA-AH class 1 antigen (AA at 30)	(AF017310) MHC class 1 antigen	(AF017309) MHC class 1 antigen	(AF012767) MHC class I antigen I-ILA-A heavy chain
Peptide C terminus Free Acid (O II)	Result Summary	# Unmatched fons	7	7	7	7	7	2	7	7	7	<b>7</b>
			JAASQR(M)	JAASQR(M)	JAASQR(M)	JAASQR(M)	JAASQR(M)	DAASQR(M)	DAASQR(M)	DAASQR(M)	DAASQR(M)	DAASQR(M)
Peptide N terminus Hydrogen (II)		Sequence	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)
Cysteines Modified by unmodified		+ 5 =					0.2948 (Y)V			0.2948 (Y)V	0.2948 (Y)V	0.2948 (Y)V
		MH+ Error (Da)	0.2948	0.2948	0.2948	0.2948	0.29	0.2948	0.2	0.2	0.2	0.2
Max. # Missed Cleavages		Calculated MH+ (Da)	1956.9052	1956,9052	1956.9052	1956.9052	1956.9052	1956.9052	1956.9052	1956.9052	1956.9052	1956.9052
Digest Used		Species	HOMO	OWOH	HOMO	HOMO	HOMO	SAPIENS	SAPIENS	SAPIENS	SAPIENS	SAPIENS HOMO SAPIENS
Max. # Peptide Masses Unmatched Ions are 5 Par(mI)Frag(av)	Parent mass. 1957.2000 (+/-500.0000pm) Fragment Ions present: [RPJV[NR][KQ]F5DR	Protein MW (Da)	21251.4	40679.8	20921.2	41113.1	18703 4	10805	18355.81	10423.4	10430 3	21027.3
		MS-Digest NCBInr.7.597 Index# Accession#	1839795	915219	825673	994765	250036	FCC0C7	786066	7204374	130100	2394322
		MS-Digest	240839	152874	141923	25035	0/165	782327	133479	49436	277806	277805
Scarch Mode Identity	Parent   Fragmen	Rank	-	. <b>-</b>	· •	- •		-	-	- •	-	

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gb/R12066/R12066 yf54d10.rl Homo sapiens cDNA clone 26062 5'similar to gb:X00492 cds 1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-3A\*0301 alpha (human); Length = 405

Plus Strand HSPs;

+5 ... Identities = 18/18 (100%), Positives=18/18(100%), Frame Score = 90 (41.9 bits), Expect = 8.1e-05, P=9.1e-05

1 VDDTQFVRFDSDAASQRM Query:

158 VDDTQFVRFDSDAASQRM VDDTQFVRFDSDAASQRM Sb)ct:

211

sapiens gb/An132653/An132653 zo21a05.rl Stratagene colon (#937204) Homo cDNA clone 587504 5' similar to gb:z46633 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 A\* 0201 ALPHA (HUMAN); Length = 428

Plus Strand RSFs:

Score = 90 (41.9) bits), Expect = 8.1e-05,P=8.ie-05 Identities = 19/18 (100%) Positives=18/18(100%) Frame Score = 90

Query: 1 VDDTQFVRFDSDAASQRM 18

VDDTQEVREDSDAASQRM Sbjct: 158 VDDTQEVREDSDAASQRM 203

gb/R59764/R59764 yh07c05.rl Homo sapiens cDNA clone 42563 5'similar to gb:x00492\_cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,A-3 A\* 0301

ALPHA (HUMAN) ;. Length = 461 Plus Strands HSPs:

Ŧ Identities - 18/18 (100%), Positives - 18/18 (100%), Erame = 90 (41.9 bits), Expect = 0.1e-05, P = 0.1e-05

Query: 1 VUUTQEVRFUSINASQRM 18

VDDTQFVRFDSDAASQRM 138 VDDTQFVRFDSDAASQRM 210

qb/Λλλ4θθ534/AAλ686534 ab37f08.rl Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 843015 5' similar to 9b:L06425 HLA CLASS I HISTOCCMPATIBILITY ANTIGEN, AW-34(A-10)) A\*3402 ALPHA (HUMAN): Length - 478

Plus Strand HSPs:

18 1 VDDTQEVRFDSDAASQRM

VDDTQFVRFDSDAASQRM Query:

138 VDDTQEVREDSDAASQRM 191 Sbjct:

Ç Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05 Identities = 18/18 (100%), Positives = 18/18 (100%),

ab/Ab548636/Ab548636 nj 38d02.sl NCI CGAP Aal Homo Saplens cDNA clone 1MACE 994755 similar to gb:z46633 HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 a\*0201 ALPHA (HUMAN); Length = 539

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Plus Strand HSPs:

Score= 30 (41.9 bits), Expect = 8.1e-05,

+ +2 -05, p = 8.1e-05 = 18/18 (100%), Frame Identities = 18/18 (100%), Positives

VDDTQFVRFDSDAASQRM 18 \_

VDDTQFVRFDSDAASQRM 205 VDDTQEVRFDSDAASQRM 152 Sbjct: gb/An147151/An147151 zo32d06.rl Stratagene colon (#937204) Homo saplens cDNA clone 5885875 similar to gb:M64740 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24 (A-9) A\*2402 AI.PHA (HUMAN); Length - 581

Plus Strands HSPs:

7 Score = 90 (41.9) bits), Expect = 8.1e-05, P = 8.1e-05 Identities = 18/18 (100%), Positives = 18/18 (100%), Frame

1 VDDTQFVRFDSDAASQRM Query:

19

13 VDDTQFVRFDSDAASQRM 66 VDDTQEVRFDSDAASQRM

gb:x00492\_cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-3A A+0301 ALPHA (HUMAN); gb/ H23377/H23377 ym57e02.rl

Length - 459

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05 Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

1 VDDTQEVREDSDAASQRM 18 Query:

VDDTQEVRFDSDAASQRH Sbjct: 154 VDDTQEVRFDSDAASQRM 207

qb/R13904/R13904 yf62c03.rl Homo sapiens cDNA clone 26801 5'similar to gb:m64742 cdsl HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) A\*2301 (HŪMAN);

Length - 459

Plus Strand HSPs:

Identities = 18/18 (100%), Positives = 18/18 (100%), Frame Score 90 (41.9 bits), Expect = 8.1e-05 P-8.1e-05

VDDTQEVREDSDAASQRM 146 VDDTQEVREDSDAASQRM 199 1 VDDTQEVRFDSDAASQRM 18 Shjct: Query:

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